

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2003, 18:28:57 ; Search time 13.1515 Seconds
(without alignments)
102.373 Million cell updates/sec

Title: US-09-743-225-9

Perfect score: 73

Sequence: 1 KDKATFGTHDGGXA 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	76.7	345	1 NBHU	apolipoprotein H p
2	46	63.0	345	1 NBMS	apolipoprotein H p
3	42	57.5	574	2 T34208	hypothetical prote
4	42	57.5	1310	2 T40135	oxysterol-binding
5	42	57.5	1674	2 T01265	starch synthase DU
6	41	56.2	297	1 NBRT	apolipoprotein H p
7	41	56.2	345	1 JN0465	apolipoprotein H p
8	40	54.8	345	1 NBBO	apolipoprotein H p
9	40	54.8	363	1 S35733	DNA-directed DNA p
10	40	54.8	1750	2 E86151	hypothetical prote
11	39	53.4	391	2 H84298	2',3'-cyclic-nucle
12	39	53.4	430	2 J28707	hypothetical prote
13	39	53.4	453	2 J27582	armadillo(arm) rep
14	39	53.4	664	2 G84771	probable acyl-CoA
15	39	53.4	1272	2 A10074	probable autotrans
16	39	53.4	1272	2 C96637	hypothetical prote
17	38	52.1	316	2 S19412	hypothetical prote
18	38	52.1	606	2 A72429	oligopeptide ABC t
19	38	52.1	616	2 E83485	probable tona-depe
20	38	52.1	1772	2 T36105	probable large gly
21	37.5	51.4	966	2 A33626	fibrinogen alpha c
22	37	50.7	160	1 S14574	globin C precursor
23	37	50.7	161	1 S14575	globin D precursor
24	37	50.7	161	1 S14576	globin E precursor
25	37	50.7	163	1 S14572	globin A precursor
26	37	50.7	216	2 D97119	amidase from nicot
27	37	50.7	537	2 S39970	glucan 1,6-alpha-g
28	37	50.7	551	2 A13601	oligopeptide trans
29	37	50.7	895	2 T34308	hypothetical prote

30	37	50.7	1354	2 AG0538	Rhs-family protein
31	37	50.7	1495	2 S27001	alpha-2-macroglobu
32	37	50.7	2089	2 C85426	ATM-like protein I
33	37	50.7	2632	2 T18718	dynein heavy chain
34	37	50.7	3738	2 T05501	hypothetical prote
35	36	49.3	242	2 S67209	hypothetical prote
36	36	49.3	307	2 G82291	glucokinase regula
37	36	49.3	376	2 AG1550	C-terminal part of
38	36	49.3	417	1 S67566	probable membrane
39	36	49.3	479	2 A25052	fibrinogen beta ch
40	36	49.3	496	2 B41322	N-acetylmuramoyl-L
41	36	49.3	585	2 AC3222	gamma-glutamyltran
42	36	49.3	798	2 S40052	glycogen phosphory
43	35.5	48.6	173	2 AB2205	hypothetical prote
44	35.5	48.6	502	2 AE1682	probable thermosta
45	35.5	48.6	502	2 AF1310	probable thermosta

ALIGNMENTS

RESULT 1

NBHU

apolipoprotein H precursor [validated] - human

N:Alternate names: activated protein C-binding protein; antidiolipin cofactor; bet

C:Species: Homo sapiens (man)

C>Date: 17-May-1985 #sequence_revision 30-Jun-1993 #text_change 08-Dec-2000

C:Accession: S17178; S17668; JQ1379; B43286; A03209; A35786; A46484; I54745; S15499;

R:Steinkasserer, A.; Estaller, C.; Weiss, E.H.; Sim, R.B.; Day, A.J.

Biochem. J. 277, 387-391, 1991

A>Title: Complete nucleotide and deduced amino acid sequence of human beta(2)-glycoprotein

A:Reference number: S17178; MUID:91315408; PMID:1650181

A:Accession: S17178

A:Molecule type: mRNA

A:Residues: 1-345 <STE>

A:Cross-references: EMBL:X58100; NID:928809; PIDN:CAA41113.1; PID:g28810

R:Kristensen, T.; Schousboe, I.; Boel, E.; Mulvihill, E.M.; Rosendahl Hansen, R.; Bac

FEBS Lett. 289, 183-186, 1991

A>Title: Molecular cloning and mammalian expression of human beta(2)-glycoprotein I c

A:Reference number: S17668; MUID:92008618; PMID:1655523

A:Accession: S17668

A:Molecule type: mRNA

A:Residues: 1-345 <KRI>

A:Cross-references: EMBL:X53595; NID:928811; PIDN:CAA37664.1; PID:g28812

R:Mehdi, H.; Nunn, M.; Steel, D.M.; Whitehead, A.S.; Perez, M.; Walker, L.; Peeples,

Gene 108, 293-298, 1991

A>Title: Nucleotide sequence and expression of the human gene encoding apolipoprotein

A:Reference number: JQ1379; MUID:92084151; PMID:1748314

A:Accession: JQ1379

A:Molecule type: mRNA

A:Residues: 1-265, 'V', 267-345 <MEH>

A:Cross-references: EMBL:X57847; NID:928813; PIDN:CAA40977.1; PID:g28814

A:Experimental source: liver

R:Nonaka, M.; Matsuda, Y.; Shirolshi, T.; Moriawaki, K.; Nonaka, M.; Natsuume-Sakai, S

Genomics 13, 1082-1087, 1992

A>Title: Molecular cloning of mouse beta-2-glycoprotein I and mapping of the gene to

A:Reference number: A33286; MUID:92372000; PMID:1339387

A:Accession: B43286

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-265, 'V', 267-345 <NON>

R:Lozier, J.; Takahashi, N.; Putnam, F.W.

Proc. Natl. Acad. Sci. U.S.A. 81, 3640-3644, 1984

A>Title: Complete amino acid sequence of human plasma beta2-glycoprotein I.

A:Reference number: A03209; MUID:84222015; PMID:6587378

A:Accession: A03209

A:Molecule type: protein

A:Residues: 20-120, 'C', 122-187, 'N', 189-265, 'V', 267-345 <LOZ>

R:McNeil, H.P.; Simpson, R.J.; Chesterman, C.N.; Krillis, S.A.

Proc. Natl. Acad. Sci. U.S.A. 87, 4120-4124, 1990

A>Title: Anti-phospholipid antibodies are directed against a complex antigen that inc

A:Reference number: A35786; MUID:90272666; PMID:2349221

A:Accession: A35786

A: Molecule type: protein
 A: Residues: 20-22, 'X', 24-37, 'X', 39-43 <MCN>
 R: Matsura, E.; Igarashi, Y.; Fujimoto, M.; Ichikawa, K.; Suzuki, T.; Sumida, T.; Yasuda, J. Immunol. 148, 3885-3891, 1992
 A: Title: Heterogeneity of anticardiolipin antibodies defined by the anticardiolipin cofactor
 A: Reference number: A46464; MUID: 922931509; PMID: 1602135
 A: Accession: A46464
 A: Molecule type: protein
 A: Residues: 20-44 <MA2>
 A: Note: sequence extracted from NCBI backbone (NCBIP:105524)
 R: Natsuura, E.; Igarashi, M.; Igarashi, Y.; Nagae, H.; Ichikawa, K.; Yasuda, T.; Koike, Int. Immunol. 3, 1217-1221, 1991
 A: Title: Molecular definition of human beta 2-glycoprotein I (beta 2-GPI) by cDNA cloning
 A: Reference number: I54745; MUID: 92135065; PMID: 1777418
 A: Accession: I54745
 A: Status: preliminary; translated from GB/EMBL/DBJ
 A: Molecule type: mRNA
 A: Residues: 1-265, 'V', 267-345 <RES>
 A: Cross-references: GB: S80305; NID: 9244677; PIDN: AAB21330.1; PID: 9244678
 C: Comment: This plasma glycoprotein is a constituent of chylomicrons, VLDL, and HDL. It is blood coagulation cascade and ADP-mediated platelet aggregation.
 C: Comment: The physiological role of this protein is uncertain. It may diminish unwanted
 C: Genetics:
 A: Gene: GDB: APOH
 A: Cross-references: GDB: 118887; OMIM: 138700
 A: Map position: 17q23-17qter
 C: Superfamily: apolipoprotein H; complement factor H repeat homology
 C: Keywords: chylomicron; duplication; glycoprotein; HDL; heparin binding; lipid binding;
 F: 1-19/Domain: signal sequence #status predicted <SIG>
 F: 20-345/Product: apolipoprotein H #status experimental <MA2>
 F: 23-79/Domain: complement factor H repeat homology <FH1>
 F: 84-137/Domain: complement factor H repeat homology <FH2>
 F: 142-200/Domain: complement factor H repeat homology <FH3>
 F: 205-260/Domain: complement factor H repeat homology <FH4>
 F: 264-325/Domain: complement factor H repeat homology <FH5>
 F: 23-66, 51-79, 110-137, 174-200, 205-248, 300-307/Disulfide bonds: #status experimental
 F: 84-124, 142-188, 234-260, 264-315, 325-345/Disulfide bonds: #status predicted
 F: 162, 183, 193, 253/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 76.7%; Score 56; DB 1; Length 345;
 Best Local Similarity 90.9%; Pred. No. 0.019;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KDKATFGTHDG 11
 ||||| |||||
 Db 227 KDKATFGCHDG 237

RESULT 2
 NBMS
 apolipoprotein H precursor - mouse
 N: Alternate names: 50K serum glycoprotein; activated protein C-binding protein; beta-2-glycoprotein I
 C: Species: Mus musculus (house mouse)
 C: Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 28-May-1999
 C: Accession: A43286; J02243
 R: Nonaka, M.; Matsuda, Y.; Shirosaki, T.; Moriaki, K.; Nonaka, M.; Natsuume-Sakai, S. Genomics 13, 1082-1087, 1992
 A: Title: Molecular cloning of mouse beta-2-glycoprotein I and mapping of the gene to chromosome 13
 A: Reference number: A43286; MUID: 92372000; PMID: 1339387
 A: Accession: A43286
 A: Molecule type: mRNA
 A: Residues: 1-252, 'A', 254-277, 'N', 279-345 <NON>
 A: Cross-references: GB: D10056
 A: Note: the authors translated the codon ACT for residue 253 as Ala and ATG for residue 254 as Met
 R: Sellar, G.C.; Steel, D.M.; Zafiroopoulos, A.; Seery, L.T.; Whitehead, A.S. Biochem. Biophys. Res. Commun. 200, 1521-1528, 1994
 A: Title: Characterization, expression and evolution of mouse beta2-glycoprotein I (apolipoprotein H)
 A: Reference number: J02243; MUID: 94242017; PMID: 7514402
 A: Accession: J02243
 A: Molecule type: mRNA
 A: Residues: 1-251, 'R', 253-345 <SEL>
 A: Cross-references: GB: S70439; NID: 9546780; PIDN: AAB30789.1; PID: 9546781

A: Experimental source: liver
 C: Genetics:
 A: Gene: B2gpl
 A: Map position: 11
 C: Superfamily: apolipoprotein H; complement factor H repeat homology
 C: Keywords: chylomicron; duplication; glycoprotein; HDL; heparin binding; lipid binding
 F: 1-19/Domain: signal sequence #status predicted <SIG>
 F: 20-345/Product: apolipoprotein H #status predicted <MA2>
 F: 23-79/Domain: complement factor H repeat homology <FH1>
 F: 84-137/Domain: complement factor H repeat homology <FH2>
 F: 142-200/Domain: complement factor H repeat homology <FH3>
 F: 205-260/Domain: complement factor H repeat homology <FH4>
 F: 264-325/Domain: complement factor H repeat homology <FH5>
 F: 23-66, 51-79, 84-124, 110-137, 142-188, 174-200, 205-248, 234-260, 264-315, 300-307, 325-345/Disulfide bonds: #status predicted
 F: 105, 117, 162, 183, 193/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 63.0%; Score 46; DB 1; Length 345;
 Best Local Similarity 80.0%; Pred. No. 1.3;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KDKATFGTHD 10
 ||||| |||||
 Db 227 KDKATFGCHE 236

RESULT 3
 T34208
 hypothetical protein F10E7.9 - Caenorhabditis elegans
 C: Species: Caenorhabditis elegans
 C: Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C: Accession: T34208
 R: Pauley, A.
 submitted to the EMBL Data Library, November 1995
 A: Description: The sequence of C. elegans cosmid F10E7.
 A: Reference number: 221489
 A: Accession: T34208
 A: Status: preliminary; translated from GB/EMBL/DBJ
 A: Molecule type: DNA
 A: Residues: 1-574 <PAU>
 A: Cross-references: EMBL: U41364; PIDN: AAB2423.1; CESP: F10E7.9
 C: Genetics:
 A: Gene: CESP: F10E7.9
 A: Introns: 37/2; 110/3; 178/1; 345/3; 468/3; 538/3

Query Match 57.5%; Score 42; DB 2; Length 574;
 Best Local Similarity 72.7%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 KDKATFGTHDG 11
 ||||| |||||
 Db 42 KDKVLFGTWDG 52

RESULT 4
 T40135
 oxysterol-binding protein homolog C2F12.05c - fission yeast (Schizosaccharomyces pombe)
 C: Species: Schizosaccharomyces pombe
 C: Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Dec-2002
 C: Accession: T40135
 R: Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
 submitted to the EMBL Data Library, June 1997
 A: Reference number: Z21907
 A: Accession: T40135
 A: Status: preliminary; translated from GB/EMBL/DBJ
 A: Molecule type: DNA
 A: Residues: 1-1310 <WOO>
 A: Cross-references: EMBL: 997211; PIDN: CAB10154.2; GSPDB: GN00067; SPDB: SPBC2F12.05c
 A: Experimental source: strain 972h; cosmid c2f12
 C: Genetics:
 A: Gene: SPDB: SPBC2F12.05c
 A: Map position: 2
 A: Introns: 20/1; 34/1; 91/3
 C: Superfamily: oxysterol-binding protein homolog OSH1/SWH1; ankyrin repeat homology;

Query Match 57.5%; Score 42; DB 2; Length 1310;
Best Local Similarity 77.8%; Pred. No. 27;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DKATFGTHD 10
I :|||||
Db 362 DNASFGTHD 370

RESULT 5
T01265
starch synthase DULL1 - maize
C:Species: Zea mays (maize)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 29-Oct-1999
C:Accession: T01265
R:Gao, M.; Wanat, J.; Stinard, P.S.; James, M.G.; Myers, A.M.
A:Title: Characterization of dull1, a maize gene coding for a novel starch synthase.
A:Reference number: Z14287; MUID:98169346; PMID:9501113
A:Accession: T01265
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1674 <GAO>
A:Cross-references: EMBL:AF023159; NID:g3057119; PIDN:AAC14014.1; PID:g3057120
C:Genetics:
A:Gene: dull1
A:Map position: 10

Query Match 57.5%; Score 42; DB 2; Length 1674;
Best Local Similarity 72.7%; Pred. No. 34;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KDKATFGTHD 11
I :|||||
Db 611 KQLATVGTGHD 621

RESULT 6
NBRT
apolipoprotein H precursor - rat
N:Alternate names: beta-2-glycoprotein I
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C:Accession: S05310
R:Aoyama, Y.; Chan, Y.L.; Wool, I.G.
Nucleic Acids Res. 17, 6401, 1989
A:Title: The primary structure of rat beta(2)-glycoprotein I.
A:Reference number: S05310; MUID:89366680; PMID:2771694
A:Accession: S05310
A:Molecule type: mRNA
A:Residues: 1-297 <AOY>
A:Cross-references: EMBL:X15551; NID:g57524; PIDN:CAA33556.1; PID:g57525
A:Note: the authors translated the codon CAA for residue 148 as Glu and GAA for residue 149.
C:Comment: This plasma glycoprotein is a constituent of chylomicrons, VLDL, and HDL and has activity, and binds heparin. It may prevent activation of the intrinsic blood coagulation cascade.
C:Superfamily: apolipoprotein H; complement factor H repeat homology <FH3>
C:Keywords: chylomicron; duplication; glycoprotein; HDL; heparin binding; lipid binding;
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-297/Product: apolipoprotein H #status predicted <NAT>
F:36-89/Domain: complement factor H repeat homology <FH1>
F:94-152/Domain: complement factor H repeat homology <FH2>
F:157-212/Domain: complement factor H repeat homology <FH3>
F:216-277/Domain: complement factor H repeat homology <FH4>
F:36-76,62-89,94-140,126-152,157-200,186-212,216-267,252-259,277-297/Disulfide bonds: #
F:114,135,145,205/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 56.2%; Score 41; DB 1; Length 297;
Best Local Similarity 70.0%; Pred. No. 8;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KDKATFGTHD 10
I :||| I :|

Db 179 KDKAVFGCHE 188

RESULT 7
JN0465
apolipoprotein H precursor - dog
N:Alternate names: beta 2 glycoprotein I
C:Species: Canis lupus familiaris (dog)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JN0465; S32693
R:Sellar, G.C.; Keane, J.; Mehdi, H.; Peeples, M.E.; Browne, N.; Whitehead, A.S.
Biochem. Biophys. Res. Commun. 191, 1288-1293, 1993
A:Title: Characterization and acute phase modulation of canine apolipoprotein H (beta 2)
A:Reference number: JN0465; MUID:93221500; PMID:7682067
A:Accession: JN0465
A:Molecule type: mRNA
A:Residues: 1-345 <SEL>
A:Cross-references: EMBL:X72933; NID:g296088; PIDN:CAA51438.1; PID:g296089
A:Experimental source: liver
C:Comment: This plasma glycoprotein is a constituent of chylomicrons, VLDL, and HDL.
C:Blood coagulation cascade and ADP-mediated platelet aggregation.
C:Superfamily: apolipoprotein H; complement factor H repeat homology <FH3>
C:Keywords: chylomicron; duplication; glycoprotein; HDL; heparin binding; lipid binding;
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-345/Product: apolipoprotein H #status predicted <NAT>
F:23-79/Domain: complement factor H repeat homology <FH1>
F:84-137/Domain: complement factor H repeat homology <FH2>
F:142-200/Domain: complement factor H repeat homology <FH3>
F:205-260/Domain: complement factor H repeat homology <FH4>
F:264-325/Domain: complement factor H repeat homology <FH5>
F:301-306/Region: phospholipid binding #status predicted
F:23-66,51-79,84-124,110-137,142-188,174-200,203-248,234-260,264-315,300-307,325-345/
F:117,162,183,193,253/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 56.2%; Score 41; DB 1; Length 345;
Best Local Similarity 70.0%; Pred. No. 10;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KDKATFGTHD 10
I :||| I :|
Db 227 KDKAMYGCHD 236

RESULT 8
NBBO
apolipoprotein H precursor - bovine
N:Alternate names: beta-2-glycoprotein I; heparin-binding protein, 46K
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Jun-1993 #sequence_revision 19-May-1995 #text_change 21-Jul-2000
C:Accession: JN0502; PN0465; S23597; A43209; A39300; S09032
R:Gao, B.; Virmani, M.; Romm, E.; Lazar-Weasley, E.; Sakaguchi, K.; Appela, E.; Kunos, Gene 126, 287-288, 1993
A:Title: Sequence of a cDNA encoding bovine apolipoprotein H.
A:Reference number: JN0502; MUID:93246260; PMID:8482546
A:Accession: JN0502
A:Molecule type: mRNA
A:Residues: 1-100, 'G', 102-107, 'S', 109-176, 'R', 178-193, 'C', 195-258, 'N', 260-301, 'N', 303
A:Cross-references: GB:L07303; NID:g162679; PIDN:AAA30382.1; PID:g162680
A:Accession: PN0465
A:Molecule type: protein
A:Residues: 20-49 <GAI>
R:Bendixen, E.; Halkier, T.; Magnusson, S.; Sottrup-Jensen, L.; Kristensen, T.
Biochemistry 31, 3611-3617, 1992
A:Title: Complete primary structure of bovine beta(2)-glycoprotein I: localization of
A:Reference number: S23597; MUID:92232647; PMID:1567819
A:Accession: S23597
A:Molecule type: mRNA
A:Residues: 4-345 <BE2>
A:Cross-references: EMBL:X60065; NID:g5; PIDN:CAA42669.1; PID:g6
A:Accession: A43209
A:Molecule type: protein
A:Residues: 20-58;63-100;108-110;124-145;150-163;174-201;203-217;228-253, 'X', 255-256,
A:Note: 186-Glu was also found

R;Kato, H.; Enjyoji, K.
 Biochemistry 30, 11687-11694, 1991
 A:Title: Amino acid sequence and location of the disulfide bonds in bovine beta2 glycoprotein
 A:Reference number: A39300; MUID:92089075; PMID:1751487
 A:Accession: A39300
 A:Molecule type: protein
 A:Residues: 20-301, N, 303-345 <KAT>
 R;Li, Q.; Blacher, R.; Esch, F.; Congote, L.F.
 Biochem. J. 267, 261-264, 1990
 A:Title: Isolation from fetal bovine serum of an apolipoprotein-H-like protein which inhibits lipoprotein lipase activity
 A:Reference number: S09032; MUID:90226328; PMID:2327984
 A:Accession: S09032
 A:Molecule type: protein
 A:Residues: 20-22, X', 24-41 <LIO>
 C:Comment: This plasma glycoprotein is a constituent of chylomicrons, VLDL, and HDL and has lipase activity, and binds heparin. It may prevent activation of the intrinsic blood coagulation system
 C:Superfamily: apolipoprotein H; complement factor H repeat homology
 C:Keywords: chylomicron; duplication; glycoprotein; HDL; heparin binding; lipid binding; lipoprotein lipase
 F:1-19/Domain: signal sequence (fragment) #status predicted <SIG>
 F:20-345/Product: apolipoprotein H #status experimental <MAT>
 F:23-79/Domain: complement factor H repeat homology <FHL>
 F:84-137/Domain: complement factor H repeat homology <FHL>
 F:142-200/Domain: complement factor H repeat homology <FHL>
 F:205-260/Domain: complement factor H repeat homology <FHL>
 F:264-325/Domain: complement factor H repeat homology <FHL>
 F:23-66, 51-79, 84-124, 110-137, 142-188, 174-200, 205-248, 234-260, 264-315, 300-325, 307-345/Disulfide bonds
 F:92,162,183,193,253/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 54.8%; Score 40; DB 1; Length 345;
 Best Local Similarity 70.0%; Pred. No. 16;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KDKATFGTHD 10
 |||||
 DB 227 KDTATFGCHE 236

RESULT 9
 S35733
 DNA-directed DNA polymerase (EC 2.7.7.7) III beta chain - Spiroplasma citri
 N:Alternate names: dnan
 C:Species: Spiroplasma citri
 C:Date: 13-Jan-1995 #sequence_revision 16-Aug-1996 #text_change 07-Dec-1999
 C:Accession: S35733
 R;Ye, F.; Laigret, F.; Bove, J.
 submitted to the EMBL Data Library, December 1992
 A:Description: Nucleotide sequence and genetic organization at the replication origin (ORI) of the plasmid pS35733
 A:Reference number: S35732
 A:Accession: S35733
 A:Molecule type: DNA
 A:Residues: 1-363 <YEF>
 A:Cross-references: EMBL:219108; NID:g49345; PIDN:CAA79522.1; PID:g49347
 C:Genetics:
 A:Gene: dnan
 A:Genetic code: SGC3
 C:Superfamily: DNA-directed DNA polymerase III beta chain
 C:Keywords: DNA replication initiation; nucleotidyltransferase

Query Match 54.8%; Score 40; DB 1; Length 363;
 Best Local Similarity 72.7%; Pred. No. 17;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KDKATFGTHD 11
 |||||
 DB 39 KDKITFTSDG 49

RESULT 10
 S86151
 Hypothetical protein F22M8.9 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
 C:Accession: S86151

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: S86151
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1750 <STO>
 A:Cross-references: GB:AE005172; NID:g8570447; PIDN:AAF76474.1; GSPDB:GN00141
 C:Genetics:
 A:Map position: 1

Query Match 54.8%; Score 40; DB 2; Length 1750;
 Best Local Similarity 77.8%; Pred. No. 83;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 KATFGTHD 11
 |||||
 DB 264 KGTFGGHDG 272

RESULT 11
 H84298
 2',3'-cyclic-nucleotide 2'-phosphodiesterase [imported] - Halobacterium sp. NRC-1
 C:Species: Halobacterium sp. NRC-1
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: H84298
 R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Laaky Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja Jung, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; A:Title: Genome sequence of Halobacterium species NRC-1.
 A:Reference number: A84160; MUID:20504483; PMID:11016950
 A:Accession: H84298
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-391 <STO>
 A:Cross-references: GB:AE004437; NID:g10580946; PIDN:AGL19756.1; GSPDB:GN00138
 C:Genetics:
 A:Gene: yfkN

Query Match 53.4%; Score 39; DB 2; Length 391;
 Best Local Similarity 77.8%; Pred. No. 27;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 DKATFGTHD 10
 |||||
 DB 10 DVATFGNHD 18

RESULT 12
 S28707
 Hypothetical protein 25 - Agrobacterium tumefaciens plasmid pTi15955
 C:Species: Agrobacterium tumefaciens
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 08-Oct-1999
 C:Accession: S28707
 R;Barker, R.F.; Idler, K.B.; Thompson, D.V.; Kemp, J.D.
 Plant Mol. Biol. 2, 335-350, 1983
 A:Title: Nucleotide sequence of the T-DNA region from the Agrobacterium tumefaciens O A:Reference number: S28683
 A:Accession: S28707
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-430 <BAR>
 A:Cross-references: EMBL:X00493; NID:g39062; PIDN:CAZ25187.1; PID:g39087

C:Genetics:

A:Genome: plasmid
C:Superfamily: short-chain alcohol dehydrogenase homology
F:200-377/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 53.4%; Score 39; DB 2; Length 430;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 FGTHDGG 12

|||||

Db 110 FGTHEGG 116

RESULT 13

JC7582

armadillo(arm) repeat protein ALEX1 - human

C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001

C:Accession: JC7582

R:Kurochkin, I.V.; Yonemitsu, N.; Funahashi, S.; Nomura, H.

Biochem. Biophys. Res. Commun. 280, 340-347, 2001

A:Title: ALEX1, a novel human armadillo repeat protein that is expressed differentially
A:Reference number: JC7582; MUID: 21092608; PMID:11162520

C:Accession: JC7582

A:Molecule type: mRNA

A:Residues: 1-453 <KUR>

A:CROSS-references: DBJ:AB039670

C:Comment: This protein is involved in regulation of normal cell growth, cell-to-cell si
C:Genetics:

A:Gene: alex1

A:Map position: Xq21.33-q22.2

C:Keywords: tandem repeat; transmembrane protein

Query Match 53.4%; Score 39; DB 2; Length 453;
Best Local Similarity 58.3%; Pred. No. 32;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KDKATFGTHDGG 12

|:|:| |:|:|

Db 91 KEKAHSGSHSGG 102

RESULT 14

G84771

probable acyl-CoA oxidase [Imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001

C:Accession: G84771

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

C:Accession: G84771

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-664 <STO>

A:CROSS-references: GB:AE002093; NID:94263786; PIDN:AAD15446.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g35690

A:Map position: 2

C:Superfamily: acyl-CoA oxidase

Query Match 53.4%; Score 39; DB 2; Length 664;
Best Local Similarity 85.7%; Pred. No. 47;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 FGTHDGG 12

|:|:|:|

Db 313 FGSHDGG 319

RESULT 15

AI0074

Probable autotransporter protein yapF [Imported] - Yersinia pestis (strain C092)
C:Species: Yersinia pestis

C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001

C:Accession: AI0074

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.

ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel
Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AI0074

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-761 <KUR>

A:CROSS-references: GB:AL590842; PIDN:CAC89460.1; PID:915978696; GSPDB:GN00175

C:Genetics:

A:Gene: yapF

Query Match 53.4%; Score 39; DB 2; Length 761;

Best Local Similarity 64.3%; Pred. No. 54;

Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KDKATFGTHDGGXA 14

|:|:| |:|:|

Db 714 KDKTQGTFFDLGMA 727

Search completed: August 28, 2003, 18:39:07

Job time : 14.1515 secs